CLAIMS

1. A method of screening a protein for involvement in cancer comprising

i) exposing the protein to a first viral oncoprotein;

ii) assaying for interaction of the protein and the first viral oncoprotein;

iii) exposing the protein to a second viral oncoprotein; and

iv) assaying for interaction of the protein and the second viral oncoprotein

wherein interaction of the protein with the viral oncoproteins indicates that the protein is involved in cancer.

2. The method according to claim 1, wherein only those proteins that interact with the first viral oncoprotein are exposed to the second viral oncoprotein.

3. A method according to claim 1 wherein the protein is contained within a mixture of proteins which may or may not be involved in the aetiology of cancer.

4. The method according to any preceding claim, wherein the protein is derived from a tissue having a highly complex pattern of gene expression combined with a high capacity for proliferation.

5. The method of claim 4 wherein the tissue is selected from placenta , cord blood $CD34^+$ haemopoietic stem cells or foetal brain.

6. A method according to any preceding claim wherein those proteins that exhibit interaction with a viral oncoprotein are correlated with interactions with other oncoproteins.

7. A method according to any preceding claim, wherein the first and second viral oncoproteins are selected from the group comprising human papilloma virus type, 16 and 18 E6, E7 and E5 proteins, hepatitis B "X", hepatitis C "Core", SV40 large "T" and small "T", adenovirus "E1A" and "E1B", human T lymphotrophic virus types 1

and 2 "Tax", Epstein Barr virus "LMP1" and "EBNA3", JC virus large "T" and small "T"

8. A method according to claim 7, wherein the first oncoprotein is HPV 16 E6.

9. A method according to claim 7 or claim 8, wherein the second oncoprotein is "Tax".

10. A method according to any preceding claim, wherein the protein is derived from a cDNA library.

11. A method according to claim 10 wherein the primary sequence of the protein can be derived by cross reference to the nucleic acid base sequence of the parent cDNA.

12. A method according to any preceding claim additionally comprising a validation phase.

13. A method according to claim 12, wherein the validation phase comprises at least one of the following further steps:

a) analysing expression levels of a protein, indicated as being involved in cancer, in cancerous and non-cancerous tissue samples;
b) comparing the levels of expression of the protein in the cancerous and non-cancerous tissues;
c) analysing the effects of targeted antisense or siRNA oligonucleotide mediated gene silencing on the growth characteristics of transformed and non-transformed cell lines;
d) analysing the effects of constitutive or inducible expression of proteins in transformed and non-transformed cell lines;
e) analysing the effects of antibodies or intrabodies directed at one or more domains of the protein; and

f) comparing the primary amino acid sequence of the protein or parent nucleic acid base sequence with one or more databases of known sequences of other proteins to identify homology with functional domains and infer putative involvement in cancer

14. A method according to claim 12, wherein the validation step comprises analysis of nucleic acids derived from a tissue sample, tumour biopsy or cell line for the presence of mutant forms of the nucleic acids encoding a protein indicated as being involved in cancer.

15. A method according to claim 12, wherein the validation phase comprises analysis of DNA derived from a tissue sample, tumour biopsy, or cell line for the presence of mutant forms of the DNA encoding a protein indicated as being involved in cancer.

16. A method according to any preceding claim, further comprising:

v) exposing a protein identified as a protein involved in cancer according to claim 1 to a protein sample; and

vi) assaying for interaction of proteins within the sample with the protein identified as involved in cancer according to claim 1;

wherein proteins identified in step vi) are secondary protein targets involved with cancer.

17. A method according to claim 16, wherein the second protein is derived from the same tissue as the protein exposed to the viral oncoproteins.

18. A method according to any preceding claim, wherein the protein indicated to be involved with cancer is selected as a target for modulation for therapy for cancer.

19. A method according to any preceding claim, wherein the protein indicated to be involved with cancer is selected as a marker for the diagnosis of cancer.

20. A method of screening a protein sample to identify proteins that are secondary protein targets for viral oncoproteins comprising:

i) exposing protein identified as a protein involved in cancer according to claim 1 to the protein sample; and

ii) assaying for interaction of proteins within the sample with proteins identified by their interaction with viral oncoproteins according to claim 1;

wherein proteins identified by their interaction with the protein involved in cancer in step ii) represent secondary protein targets involved with cancer.

21. The method of claim 20 further comprising the step of :

iii) Investigating the functional validation of the secondary targets in cancer by the according to the steps defined by claim 13.